Set to Version 1
) [illegible] 2000 [illegible]

Initial Sm Model

[illegible]:40 ; Scan time: [illegible] Seconds
(Minimal [illegible] comments)
[illegible]% Minimum cell updates/sec

[illegible]

Database: DB

Maximum 1.0

Published Residues

DB: Custom parameters [illegible]:44

[illegible]

Searched:
[illegible]
Summaries

[illegible]*
1data1/p[illegible]/pa[illegible]:* 1.SEQ:*
1data1/patseq1/pa[illegible]:* 2.SEQ:*
1data1/p[illegible]:* 3.SEQ *
1data1/p[illegible]:* 4.SEQ:*
1data1/genseq1/g[illegible]:* 5.SEQ:*
1data1/g[illegible]:* 6.SEQ:*
1data1/p[illegible]:* 7.SEQ:*
1data1/genseq1/g[illegible]:* 8.SEQ:*
1data1/g[illegible]:* 9.SEQ:*
2pdata1/p[illegible]:* 1.SEQ:*
2pdata1/p[illegible]:* 2.SEQ *
2pdata1/g[illegible]:* 3.SEQ *
2pdata1/g[illegible]:* 4.SEQ:*
2pdata1/g[illegible]:* 5.SEQ:*
2pdata1/g[illegible]:* 6.SEQ:*
2pdata1/g[illegible]:* 7.SEQ:*
2pdata1/g[illegible]:* 8.SEQ:*
2pdata1/g[illegible]:* 9.SEQ:*
2pdata1/g[illegible]:* 10.SEQ:*
2pdata1/g[illegible]:* 11.SEQ:*
2pdata1/g[illegible]:* 12.SEQ:*
2pdata1/g[illegible]:* 13.SEQ:*
2pdata1/g[illegible]:* 14.SEQ:*
2pdata1/g[illegible]:* 15.SEQ:*
2pdata1/g[illegible]:* 16.SEQ:*

[illegible] 2 results predicted [illegible] have a
[illegible] to the score [illegible] result being printed.
[illegible] the total [illegible] distribution.

SUMMARIES

[illegible]	[illegible]					Description
	1	X86576				PCR primer for hum
	2	A58549				PCR primer used to
	3	[illegible]				Primer #3 for cDNA
	4	[illegible]				Primer #4 for cDNA
	5	[illegible]				Human gene signatu
	6	V23814				Primer KAN-2 for N
	7	V22991				Primer KAN-2 used
	8	[illegible]				Plasmid constructi
	9	AL2372				Plasmid pKTK40 Km
	10	[illegible]				Human beta globin
	11	A77417				Human clone cq4494
	12	12.8	71.1	76	19	V41383	Nested PCR primer
	13	12.4	68.9	24	21	A57941	Sense PCR primer f
	14	12.4	68.9	50	16	Q94415	[illegible] NBZ RNA fi
c	15	12.2	67.8	50	19	V49704	Human J chain targ
c	16	12.2	67.8	50	20	X08857	Nucleotide used to
	17	12.2	67.8	54	18	X62731	Granule bound stat
	18	12.2	67.8	60	16	T00252	Thrombin 60N DNA l
c	19	12.2	67.8	62	19	V49706	Human J chain targ
c	20	12.2	67.8	62	19	V45309	Targeting molecule
c	21	12.2	67.8	62	20	X08859	Nucleotide used in
	22	12.2	67.8	69	19	V49705	Human J chain targ
	23	12.2	67.8	69	20	X08858	Nucleotide used to
	24	12.2	67.8	81	19	V49707	Human J chain targ
	25	12.2	67.8	81	19	V45310	Targeting molecule
	26	12.2	67.8	81	20	X08860	Nucleotide used in
c	27	12.2	67.8	94	16	T26403	Human gene signatu
c	28	12	66.7	23	20	X00943	B. pertussis bpHi
c	29	12	66.7	27	20	X00937	B. pertussis bpHi
c	30	11.8	65.6	18	21	A58499	PCR primer used to
c	31	11.8	65.6	21	20	X27526	Bovine FEL gene fr
	32	11.8	65.6	31	21	A78761	Human genomic DNA
	33	11.8	65.6	35	16	T05676	Schistosoma mansoni
	34	11.8	65.6	44	14	Q42165	hCH-SIP 1 (7-37) f
c	35	11.8	65.6	44	14	Q42166	hCH-SIP 1 (7-37) f
	36	11.8	65.6	45	20	Z33934	Human PRO429 hybri
	37	11.8	65.6	45	21	Q78631	Human PRO429 hybri
c	38	11.8	65.6	73	16	T21163	Human gene signatu
	39	11.8	65.6	78	20	X16096	PCR primer used to
c	40	11.8	65.6	78	20	X16097	PCR primer used to
	41	11.6	64.4	20	20	Z05959	PCR primer used to
c	42	11.6	64.4	30	19	V33162	Nucleotide sequenc
c	43	11.6	64.4	42	18	T65560	oligonucleotide 12
c	44	11.6	64.4	62	18	I04641	orfST receptor pro
c	45	11.6	64.4	62	19	V55466	Granulocyte colony

ALIGNMENTS

RESULT 1
[illegible]
ID A95[illegible] standard; DNA; 22 BP.
XX
AC X95[illegible];
XX
DT 07-JUN-1999 (first entry)
XX
DE [illegible]'s primer for human bAG-3 coding sequence.
XX
KW EDG-1; EDG-2; EDG-3; EDG-4; EDG-5; PSP 24; human; detection; therapy;
KW Edg-3 agonist, allosteric modulator, lysophosphatidic acid receptor;
KW LPA signalling; mediated disease; ciliar apoptosis; [illegible]'s primer, ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9919513-A2.
XX
PD 22-APR-1999.
XX
PF 09-OCT-1998; 98WO-US21315.
XX
PR 10-OCT-1997; 97US-0061572.
XX
PA (LEXB-) LEXICON GENETICS INC
XX
PI Erikson J, Goddard JG, Kieter M;
XX
DR WPI; 1999-277658/24.
XX
PT Identification of (ant)agonists of LPA receptor EDG-2 for, e.g.
PT treating LPA signalling mediated diseases such as ciliar apoptosis
XX

PS Example 1; Page 30; 63pp; English.
XX
CC This sequence is a PCR primer for DNA encoding human EDG-4.
CC The invention relates to methods of detecting (ant)agonist, inverse
CC agonist or allosteric modulators of the lysophosphatidic acid receptors
CC EDG-1, EDG-2, EDG-3, EDG-4, EDG-5, and PSP-24. The methods are used to
CC identify (ant)agonists and allosteric modulator of the lysophosphatidic
CC acid (LPA) EDG2 receptor, e.g. to treat LPA signalling mediated disease
CC such cellular apoptosis.
XX
SQ Sequence 42 BP; 5 A; 14 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cqqqaqgcaqttqccat 18
||||||||||||||||||
Db 42 CGGGAGGGCAGTTGCCAT 25

RESULT 2
A58539/c
ID A58539 standard; DNA; 18 BP.
XX
AC A58539;
XX
DT 20-OCT-2000 (first entry)
XX
DE PCR primer used to amplify bleomycin (BLM) gene cluster OKF40.
XX
KW BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
KW bleomycin; bleomycin analogue; holo carrier protein; thiazolidine;
KW thiazoline; bithiazoline; microbial metabolite; sugar; PCR primer; ss.
XX
OS Streptomyces verticillus.
XX
PN WO200040704-A1.
XX
PD 13-JUL-2000.
XX
PF 06-JAN 2000; 2000WO-US00445.
XX
PR 06-JAN-1999; 99US-0115435.
PR 05-FEB-1999; 99US-0118848.
PR 05-JAN-2000; 2000US-0477962.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Shen B, Du L, Sanchez C, Chen M, Edwards DJ;
XX
DR WPI; 2000-465974/40.
XX
PI New bleomycin gene cluster components useful for peptide and/or
PT polyketide metabolites, especially bleomycin, production and for
PT chemically modifying biological molecules -
XX
PS Disclosure; Page 24; 167pp; English
XX
CC PCR primers A58474-A58541 were used to amplify open reading frames
CC (ORFs) 8 to 41 of the BLM (Bleomycin) gene cluster. The proteins encoded
CC by the gene cluster are useful for producing peptides and/or polyketide
CC metabolites, especially bleomycin or bleomycin analogues. They are
CC also useful for chemically modifying biological molecules to produce
CC branched methyl groups, and for coupling amino acids and fatty
CC acids. They may be reacted with an apo carrier protein and coenzyme A
CC to produce a holo-carrier protein. The BLM gene cluster or catalytic
CC domains can be used individually or collectively to produce
CC thiazolidine, thiazoline, bithiazoline and bithiazoline-containing
CC microbial metabolites. The BLM gene cluster may also be used to produce
CC sugars.
XX

SQ Sequence 18 BP; 2 A; 12 C; 3 G; 1 T; 0 other;

Query Match 74.4%; Score 13.4; DB 21; Length 18;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 qqqaaqqcaqttqcc 16
||||||| ||||||
Db 18 GGGAGGGCGGTTGCC 4

RESULT 3
T39057/c
ID T39057 standard; cDNA; 57 BP.
XX
AC T39057;
XX
DT 20-MAY-1997 (first entry)
XX
DE Primer #3 for cDNA encoding cellulytic enzyme.
XX
KW Cellulytic enzyme; endoglucanase; hydrolysis; cellulose; microorganism;
KW plant cell wall; catalytic region; textile; fabrication; bio polishing;
KW stone washing; cellulosic fabric; colour clarification; defibration; PCR;
KW cell wall degradation; paper pulp; debarking; fibre modification; primer;
KW enzymatic de-inking; drainage improvement; polymerase chain reaction;
KW amplify; ss.
XX
OS Synthetic.
XX
PN WO9629397-A1.
XX
PD 26-SEP-1996.
XX
PF 18-MAR-1996; 96WO-DK00105.
XX
PR 12-FEB-1996; 96DK-0000137.
PR 17-MAR-1995; 95DK-0000272.
PR 08-AUG-1995; 95DK-0000885.
PR 08-AUG-1995; 95DK-0000886.
PR 08-AUG-1995; 95DK-0000887.
PR 08-AUG-1995; 95DK-0000888.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Andersen LN, Ihara M, Kauppinen MS, Lange L, Lassen SF;
PI Nielsen RI, Schuelein M, Takagi S;
XX
DR WPI; 1996-443173/44.
XX
PT New endo-glucanase enzyme preparations - contg. conserved catalytic
PT regions, useful for treating fabrics, textiles, plant material or
PT paper pulp
XX
PS Example 1; Page 104; 316pp; English.
XX
CC T39055-T39060 represent amplification primers for the coding sequence of
CC [illegible] of the invention. These sequences are specifically used to
CC amplify the Myceliophthora thermophila endoglucanase coding sequence (see
CC T39047). The encoded enzymes possess cellulytic (particularly
CC endoglucanase) activity. Cellulytic enzymes are involved in the the
CC hydrolysis of cellulose, and are synthesised by a large number of
CC microorganisms and plants. The enzymes of the invention containing the
CC conserved catalytic regions (such as W09419) exhibit improved
CC performance, e.g. 50 times higher performance, compared to multiple
CC domain enzymes. The enzymes can be used for the treatment of fabrics or
CC textiles, preferably for preventing backstaining, for bio polishing or
CC for stone washing cellulosic fabric. They can also be used to provide
CC colour clarification for laundry. The enzymes can also be used for the
CC degradation or modification of plant material, such as cell walls. They
CC can also be used in the treatment of paper pulp preferably for debarking,
CC defibration, fibre modification, enzymatic de-inking or drainage

```
                ... 16 G; 8 T; ... other;

            %;  Score 13.2;  DB ...;  Length 57;
            %;  Pred. No. ...
                ;  Mismatches   ...   Indels   0;  Gaps   0;

            18

            ... BG

            ...)

            ...and cellulytic en...

            ...ctinase; hydrol...; microorganism;
            ...tion; textile; ...; bio-polishing;
            ...; defibration; PCR;
            ...aper pulp; debarking; ...ification; primer;
            ...inage improvement; polymerase chain reaction;

            ...
            ...
            887.
            888.

            Kauppinen MS; ...; ... SF;
            ... Tikhin S;

            ...preparations ... catalytic
            ...ing fabrics, textile ... material or

            ...pp; English.

            ...ification provides the coding sequence of
            ... These sequences are specifically used to
            ...a thermophila endo...nase coding sequence (see
            ...zymes possess cellul... (particularly
            ... Cellulytic enzymes are involved in the the
            ...and are synthesised ... large number of
            ...s. The enzymes of the invention containing the
            ...ons (such as WO...) exhibit improved
            ...es better performance compared to multiple
            ...zymes can be used for the treatment of fabrics or
            ... preventing backstaining, for bio-polishing or
            ...ose fabric. They can also be used to provide
            ... laundry. The enzymes can also be used for the
            ...tion of plant material such as cell walls. They
```

```
CC   can also be used in the treatment of paper pulp preferably for debarking,
CC   defibration, fibre modification, enzymatic de-inking or drainage
CC   improvement.
XX
SQ   Sequence 57 BP; 8 A; 16 C; 22 G; 11 T; 0 other;

  Query Match              73.3%;  Score 13.2;  DB 17;  Length 57;
  Best Local Similarity    83.3%;  Pred. No. 8.1e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         1 cggaggacagttaccat 18
             ||| || | ||||||| |
Db         1 cggcaggaagttaccat 18

RESULT    5
I23705
ID   I23705 standard; cDNA to mRNA; 65 BP.
XX
AC   I23705;
XX
DT   12-SEP-1996  (first entry)
XX
DE   Human gene signature HUMGS05581.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP01916.
XX
PR   12-NOV-1993;   93JP-0355564.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Identifying gene signatures in 3'-directed human cDNA library - used
PT   for diagnosis of abnormal cell function, by preparing cDNA that
PT   reflects relative abundance of corresp. mRNA in specific human
PT   tissues
XX
PS   Claim 1; Page 1434; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp.
CC   double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC   given in I19001-I26837 and which is able to hybridise to part of
CC   human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC   sequences were obtained from 3'-directed cDNA libraries prepared
CC   from various human tissues; synthesis of cDNA was initiated from the
CC   3'-end of mRNA by using poly(T) as the sole primer. Since the 3'
CC   untranslated sequence is unique to a particular mRNA species, almost
CC   all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC   is constructed so as to reflect accurately the relative abundance of
CC   different mRNAs in the particular tissue from which it was derived.
CC   The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS
CC   sequences) as a means of diagnosing abnormal cell function or for
CC   recognising different cell types.
XX
SQ   Sequence 65 BP; 22 A; 13 C; 17 G; 12 T; 1 other;
```

```
  Query Match             74.3%;  Score 13.2;  DB 16;  Length 65;
  Best Local Similarity   83.3%;  Pred. No. 8.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 cqqqaqqqcaqttqccat 18
           ||| |||| ||| |||||
Db      11 cqqqaqqqaagtaqccat 28


RESULT   6
V23814/c
ID   V23814 standard; DNA; 27 BP.
XX
AC   V23814;
XX
DT   29-JUL-1998  (first entry)
XX
DE   Primer KAN-2 for Nitrosomonas dnaK gene promoter.
XX
KW   Heatshock promoter; dnaK gene; stress sensing probe; oxidative stress;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Nitrosomonas europaea.
XX
PN   JP10108678-A.
XX
PD   28-APR-1998.
XX
PF   07-OCT-1996;   96JP-0266320.
XX
PR   07-OCT-1996;   96JP-0266320.
XX
PA   (KURK ) KURITA WATER IND LTD.
XX
DR   WPI; 1998-304473/27
XX
PT   New heat-shock promoter from Nitrosomonas species - useful for, e.g.
PT   measuring oxidative stress caused by ammonia
XX
PS   Example 1; Page 8; 18pp; Japanese.
XX
CC   This sequence is a primer for the dnaK gene promoter of Nitrosomonas
CC   europaea. The heat-shock promoter (HP) of the amplified DNA is an example
CC   of the promoter of the invention. The HP can be used in a stress sensing
CC   gene comprising: (a) a fused DNA fragment comprising HP, and (b) a DNA
CC   fragment positioned downstream of the fragment of (a), comprising a
CC   structural gene encoding a protein for detecting a gene expression. A
CC   microorganism carrying the stress-sensing gene may be used to measure the
CC   oxidative stress caused by ammonia, by culturing it and measuring the
CC   expression of the stress-sensing gene. The method can measure the
CC   oxidative stress easily and rapidly.
XX
SQ   Sequence 27 BP; 4 A; 10 C; 9 G; 4 T; 0 other;


  Query Match             71.1%;  Score 12.8;  DB 19;  Length 27;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 cqqqaqqqcaqttqcc 16
           |||| |||| |||| ||
Db      16 CGGGACGGCAGCTGCC 1


RESULT   7
V22991/c
ID   V22991 standard; DNA; 27 BP.
XX
AC   V22991;
XX
DT   30-JUL-1998  (first entry)
XX
DE   Primer KAN-2 used to amplify the kanamycin acetyl transferase gene.
XX
KW   kanamycin acetyl-transferase gene; inhibition; nitrifying activity;
KW   ammonia oxidising bacteria; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   EP0835940-A1.
XX
PD   15-APR-1998.
XX
PF   08-OCT-1997;   97EP-0117365.
XX
PR   08-OCT-1996;   96JP-0267053.
XX
PA   (KURK ) KURITA WATER IND LTD.
XX
PI   Iizumi T;
XX
DR   WPI; 1998-224125/19.
XX
PT   Detecting inhibition of nitrifying activity of ammonia-oxidising
PT   bacteria - using recombinant bacterium containing luciferase
PT   reporter gene construct
XX
PS   Disclosure; Page 7; 19pp; English.
XX
CC   PCR primers V22990-91 were used to amplify the
CC   kanamycin acetyl transferase gene of TB999. The amplified sequence was
CC   used to create a construct that is used to inhibit the nitrifying
CC   activity of ammonia-oxidising bacteria. The method comprises transforming
CC   an ammonia oxidising bacterium with a DNA construct that contains a
CC   luciferase gene under the control of a promoter capable of initiating
CC   expression of the luciferase gene under conditions where nitrification
CC   occurs in the bacterium. A sample solution is incubated with a culture
CC   of the recombinant bacterium and visible light emission, catalysed by
CC   the luciferase, is measured.
XX
SQ   Sequence 27 BP; 4 A; 10 C; 9 G; 4 T; 0 other;


  Query Match             71.1%;  Score 12.8;  DB 19;  Length 27;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 cqqqaqqqcaqttqcc 16
           |||| |||| |||| ||
Db      16 CGGGACGGCAGCTGCC 1


RESULT   8
C64689/c
ID   C64689 standard; DNA; 27 BP.
XX
AC   C64689;
XX
DT   27-FEB-2001  (first entry)
XX
DE   Plasmid construction PCR primer Kan 1 PCR ID NO:12.
XX
KW   Nitrosomonas europaea; tipX; TRPA-1; TRPA 2; frozen microbe body;
KW   ammonia oxidising microbe; inhibition; nitrification; luciferase;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP2000262269-A.
XX
PD   26-SEP-2000.
XX
PF   15-MAR-1999;   99JP-0067954.
XX
PR   15-MAR-1999;   99JP-0067954.
```

[illegible]

[illegible] ammonia oxidising microbe
[illegible] ful for [illegible] the inhibiting rate
[illegible]

[illegible] purposes.

[illegible] describes a method for the preparation of the
[illegible] monia oxidising state in which a
[illegible] ding a protein which affects the bioluminescence
[illegible] oxidising microbe, e.g. a luciferase gene and
[illegible] bility to a biological inhibiting substance
[illegible] the ammonia oxidising ability is frozen.
[illegible] ing microbe body [illegible] ammonia oxidising microbe
[illegible] monia-oxidising microbe including luciferase gene
[illegible] the above protection agent, the frozen microbe
[illegible] measurement of the inhibition rate on
[illegible] the present sequence represents a PCR primer.
[illegible] mple from the present [illegible].

[illegible]

[illegible] Score 12.8, [illegible] ength 27;
[illegible] Prod. No. 1 [illegible]
[illegible] Mismatches [illegible] Indels 0; Gaps 0;

[illegible]

[illegible]

[illegible]

[illegible]

[illegible] KAN 2.

[illegible] oxidising [illegible] inhibitor;
[illegible] ing a [illegible] kanamycin [illegible] PCR primer; ss.

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible] ing microbe body [illegible] oxidizing
[illegible] ing treatment [illegible]

[illegible] manure.

[illegible] The method [illegible] preparation of a
[illegible] position, which comprises an ammonia-oxidizing
[illegible] bic, where the [illegible] activity of the
[illegible] a protein that guards the ability to respond to
[illegible] stance, the ammonia-oxidizing microbe is

CC used for the treatment of waste water. The method can improve storage
CC stability of the microbe body. This sequence represents a PCR primer used
CC in the amplification of the kanamycin resistance Km R gene isolated from
CC plasmid pKJK4c which is used to illustrate the method of the invention.
XX
SQ Sequence 27 BP; 7 A; 10 C; 9 G; 4 T; 0 other;

Query Match 71.1%; Score 12.8; DB 21; Length 27;
Best Local Similarity 87.5%; Prod. No. 1 [illegible];
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cqqqaqqqcaattgcc 16
|||||:|||:|||
Db 16 CGGGACGGCAGCTGCC 1

RESULT 13
Q36348
ID Q36348 standard; DNA; 39 BP.
XX
AC Q36348;
XX
DT 07-JUN-1993 (first entry)
XX
DE Human beta-globin 5' enhancer target sequence.
XX
KW Haemoglobin; beta thalassemia; sickle cell anaemia; delta protein;
KW triplex; target; duplex; promoter; coding domain; ss.
XX
OS Synthetic.
XX
PN US5176996-A.
XX
PD 05-JAN-1993.
XX
PF 20-DEC-1988; 88US-0287459.
XX
PR 20-DEC-1988; 88US-0287459.
PR 22-DEC-1989; 89US-0454532.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Hogan ME, Kessler DJ;
XX
DR WPI; 1993-035718/04.
XX
PT Synthetic oligonucleotide(s), prodn. useful e.g. in gene
PT inhibition - which bind to target sequence in duplex DNA forming
PT colinear triplex by binding to major groove
XX
PS Example 14; Column 34; 29pp; English.
XX
CC The beta globin gene encodes one of the proteins comprising human
CC adult haemoglobin. Mutation in this gene is responsible for beta
CC thalassemia and sickle cell anaemia. Expression of the gene may be
CC prevented by the formation of a triplex between the duplex target DNA
CC sequence and an anti parallel or parallel synthetic oligonucleotide.
CC The triplex oligonucleotides are designed to inhibit the beta
CC globin gene in thallassemics and in patients with sickle cell anaemia,
CC to be replaced by the naturally occurring delta protein. Two classes
CC of triplex oligonucleotides may be used, targetted against the 5'
CC enhancer or the promoter/coding domain, in this case from base -63
CC to -25 (numbering is relative to the principal mRNA start site).
CC See also Q36219-362.
XX
SQ Sequence 39 BP; 12 A; 6 C; 19 G; 2 T; 0 other;

Query Match 71.1%; Score 12.8; DB 34; Length 39;
Best Local Similarity 87.5%; Prod. No. 1 [illegible];
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2 qqqaqqqcaqttqcca 17
           ||||||||||  ||||
Db       8 qqqaqqqcaqqaqcca 23


RESULT  11
A77417
ID   A77417 standard; cDNA; 51 BP.
XX
AC   A77417;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human clone cq44938456 polymorphic site, SEQ ID N:1180.
XX
KW   Human; single nucleotide polymorphism; SNP; chromosome 2;
KW   detection; identification; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/qualifiers
FT   variation       replace (26,A)
FT                   /*tag= a
XX
PN   WO200029623-A2.
XX
PD   25-MAY-2000.
XX
PF   17-NOV-1999;    99WO-US27293.
XX
PR   17-NOV-1998;    98US-0109024.
PR   16-NOV-1999;    99US-0109024.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA, Leach MD;
XX
DR   WPI; 2000-387826/33.
XX
PT   Human nucleic acids containing single nucleotide polymorphisms, useful
PT   for treating a subject suffering, or at risk from a pathology due to
PT   the presence of a sequence polymorphism.
XX
PS   Claim 1; Page 490; 543pp; English.
XX
CC   Sequences A76318-A77509 represent 1192 human nucleic acid sequences
CC   which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC   1112 (A76318-A77429) are consecutive pairs of nucleotides which contain
CC   silent SNPs. Sequences 1113 to 1192 (A77430-A77509) are consecutive pairs
CC   of nucleotides containing SNPs which result in changes in the
CC   corresponding amino acid sequences (B11749-B11828). The SNPs in sequences
CC   1113 to 1128 (A77430-A77445) lead to conservative amino acid changes,
CC   while those in sequences 1129 to 1186 (A77446-A77503) result in non
CC   conservative changes. The SNPs in sequences 1187 to 1192 (A77504-A77509)
CC   generate frameshift mutations. The invention also relates to a method of
CC   detecting a polymorphic site in a nucleic acid and a method of
CC   determining the relatedness of two nucleic acids. It also encompasses
CC   peptides containing polymorphic sites, antibodies raised against such
CC   peptides, and a method of detecting polymorphic proteins/peptides using
CC   the antibodies. The nucleic acids are useful for gene therapy of an
CC   individual having, suspected of having, or at risk of developing a
CC   pathological condition due to the presence of a sequence polymorphism.
CC   Such treatment would comprise administration of the wild type nucleic
CC   acid sequence. Antibodies raised against polymorphic peptides can also
CC   be used in the treatment of such individuals.
XX
SQ   Sequence 51 BP; 12 A; 13 C; 17 G; 9 T; 0 other;

  Query Match             71.1%;  Score 12.8;  DB 21;  Length 51;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 qqqaqqqcaqttqcca 17
           || || ||||||||||
Db      20 qacaqcqcaqttqcca 35


RESULT  12
V41383
ID   V41383 standard; DNA; 76 BP.
XX
AC   V41383;
XX
DT   08-OCT-1998  (first entry)
XX
DE   Nested DNA fragment #1.
XX
KW   DNA fractionation; sequencing; protein affinity assay; modification;
KW   universal diagnostic chip; antibody screening; cloning; mapping; ss.
XX
OS   Synthetic.
XX
PN   WO9827229-A1.
XX
PD   25-JUN-1998.
XX
PF   16-DEC-1997;    97WO-US23242.
XX
PR   17-DEC-1996;    96US-0768803.
XX
PA   (UYCH-) UNIV CHICAGO.
XX
PI   Dubiley SA, Lysov YP, Mirzabekov AD;
XX
DR   WPI; 1998-362796/31.
XX
PT   Affinity fractionation and sequencing of DNA using arrays of
PT   complementary oligo:nucleotide(s) and multi step conversion or
PT   manipulation of nanolitre samples in polyacrylamide vessels, e.g.
PT   for antibody screening.
XX
PS   Disclosure; Fig 3; 28pp; English.
XX
CC   This represents a nested DNA fragment used to exemplify the methods of
CC   invention of affinity fractionation and sequencing of DNA. One method
CC   comprises cleaving DNA into fragments of predetermined length, labelling
CC   the fragments and hybridising them to an array of isolated
CC   oligonucleotides complementary to parts of the DNA. Fragments that have
CC   hybridised are recovered and hybridised to a second array of immobilised
CC   oligonucleotides, some of which are complementary to the hybridised
CC   fragments. Labelled oligomers complementary to the hybridised fragments
CC   that have re-hybridised to the second array are attached. The invention
CC   also provides a method for performing multi-step conversion of compounds
CC   by adding the compounds to each vessel in an array of polyacrylamide
CC   vessels (each vessel containing a single immobilised reactant) in a
CC   predetermined sequence. After reaction, converted compounds from the
CC   array are isolated. A second method for manipulating nanolitre quantities
CC   of compounds comprises removeably attaching compounds to a polyacrylamide
CC   vessel having volume from a fraction to several hundred nanolitre,
CC   modifying the compound while confined in the vessel and recovering
CC   modified products. These methods can be used for DNA fractionation/
CC   sequencing or in protein affinity assays, e.g. for constructing a
CC   universal diagnostic chip for antibody screening. DNA sequencing can now
CC   be done without costly cloning and mapping stages. The second method
CC   allows many fractionation/modification reactions (including multi step
CC   conversions) to be performed simultaneously and in a site specific
CC   manner.
XX
SQ   Sequence 76 BP; 19 A; 19 C; 28 G; 10 T; 0 other;

  Query Match             71.1%;  Score 12.8;  DB 19;  Length 76;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

ID Q93315 standard; RNA; 50 BP.
XX
AC Q93315;
XX
DT 14-AUG-1996 (first entry)
XX
DE bFGF 2'-NH2 RNA ligand 26B.
XX
KW Family 1; family 2; ligands; basic fibroblast growth factor; bFGF;
KW systematic evolution of ligands by exponential enrichment; SELEX;
KW heparin selection; region of homology; inhibitor; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified base 1..50
FT /*tag = a
FT /mod_base= c - 2' NH2 cytosine
FT /mod_base= u - 2'-NH2 uracil
XX
PN WO9521853-A1.
XX
PD 17-AUG-1995.
XX
PF 06-FEB-1995; 95WO-US01458.
XX
PR 28-MAR-1994; 94US-0219012.
PR 10-FEB-1994; 94US-0195005.
PR 11-JUN-1990; 90US-0536428.
PR 10-JUN-1991; 91US-0714131.
PR 22-APR-1993; 93US-0061691.
XX
PA (NEXS) NEXSTAR PHARM INC.
XX
PI Gold L, Janjic N, Tasset D;
XX
DR WPI; 1995-293073/38.
XX
PT Identification of ligands to basic fibroblast growth factor and
PT thrombin - which can be modified for increased in vivo stability
XX
PS Claim 17; Page 85; 236pp; English.
XX
CC The sequences given in Q93258-342 represent a group of 2' NH2 RNA
CC ligands to basic fibroblast growth factor (bFGF). These sequences
CC represent the fragment in the consensus sequence given in Q93345.
CC These ligands were isolated using systematic evolution of ligands by
CC exponential enrichment (SELEX). The selection was conducted in PBS
CC at 37 deg. C in the presence of heparin which competes with the RNA
CC for binding to bFGF. The starting ligand pools contained 2'-NH2
CC modified RNA which has improved stability. After twelve rounds of
CC selection, the RNA pools showed a definite departure from randomness,
CC the affinity of the modified RNA pools was improved by 1-2 orders of
CC magnitude. Individual members of the enriched pools were then cloned
CC into pUC18 and sequenced. Distinct families were identified based on
CC overlapping regions of homology (see also Q93258-76). A number of
CC sequences showed homology to two families (see also Q93295-303) and
CC some sequences showed no obvious homology to any of the families
CC (see also Q93304-22). One family of ligands bound nitrocellulose
CC (see also Q93323-42). These ligands are inhibitors of bFGF and are
CC therefore useful in treating bFGF mediated conditions and in studying
CC the structure and binding of bFGF.
XX
SQ Sequence 50 BP; 7 A; 11 C; 18 G; 14 U; 0 other;

Query Match 68.0%; Score 12.4; DB 16; Length 50;
Best Local Similarity 85.7%; Prod. No. 2e-03;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cqqqaqqqcaqttq 14
|||||||||||:|
Db 14 cqqqaqqqcaqaaq 27

```
RESULT 15
V49704/c
ID   V49704 standard; DNA; 50 BP.
XX
AC   V49704;
XX
DT   04-NOV-1998 (first entry)
XX
DE   Human J chain target molecule DNA oligonucleotide 15.
XX
KW   Target; imaging agent; epithelium; transepithelia. transport; diagnosis;
KW   transcytosis, disease; basolateral; internalisation; J chain; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9830591-A1.
XX
PD   16-JUL-1998.
XX
PF   09-JAN-1998;   98WO-US00339.
XX
PR   10-JAN-1997;   97US-0782480.
XX
PA   (EPIC-) EPICYTE PHARM INC.
XX
PI   Fitchen JH, Bein MB, Hiatt AC;
XX
DR   WPI; 1998-399066/34.
XX
PI   New epithelial tissue targeting agent used to deliver imaging
PI   agents to an epithelial surface for internalisation; useful in
PI   diagnosis
XX
PS   Example 1c; Page 100; 118pp; English.
XX
CC   V49672-V49715 are oligonucleotides used in a method resulting in the
CC   construction of a target molecule from human J chain protein fragments.
CC   This construct is used in a method to target imaging agents to epithelial
CC   surfaces at which they may remain or undergo transepithelial transport
CC   via transcytosis. At least one imaging agent is linked to the targeting
CC   molecule comprising a polypeptide that (a) forms a closed covalent loop,
CC   (b) contains at least 3, preferably 4, peptide domains having beta-sheet
CC   character separated by domains lacking beta-sheet character and (c) is
CC   not full length dimeric IgA. The imaging agents are useful in the
CC   diagnosis of disease. The target molecule is also capable of specifically
CC   binding to a basolateral factor associated with an epithelial surface to
CC   cause internalisation of a biological agent linked to the target
CC   molecule.
XX
SQ   Sequence 50 BP; 14 A; 14 C; 12 G; 10 T; 0 other;


  Query Match             67.8%;  Score 12.2;  DB 19;  Length 50;
  Best Local Similarity   82.4%;  Prod. No. 2.5e-03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 cqqqaqqqcaqttqcca 17
           ||  |||||||||| |||
Db      27 CGTAAGGGCAGTTTCCA 11


Search completed: May  5, 2001, 11:52:41
Job time: 6404 sec
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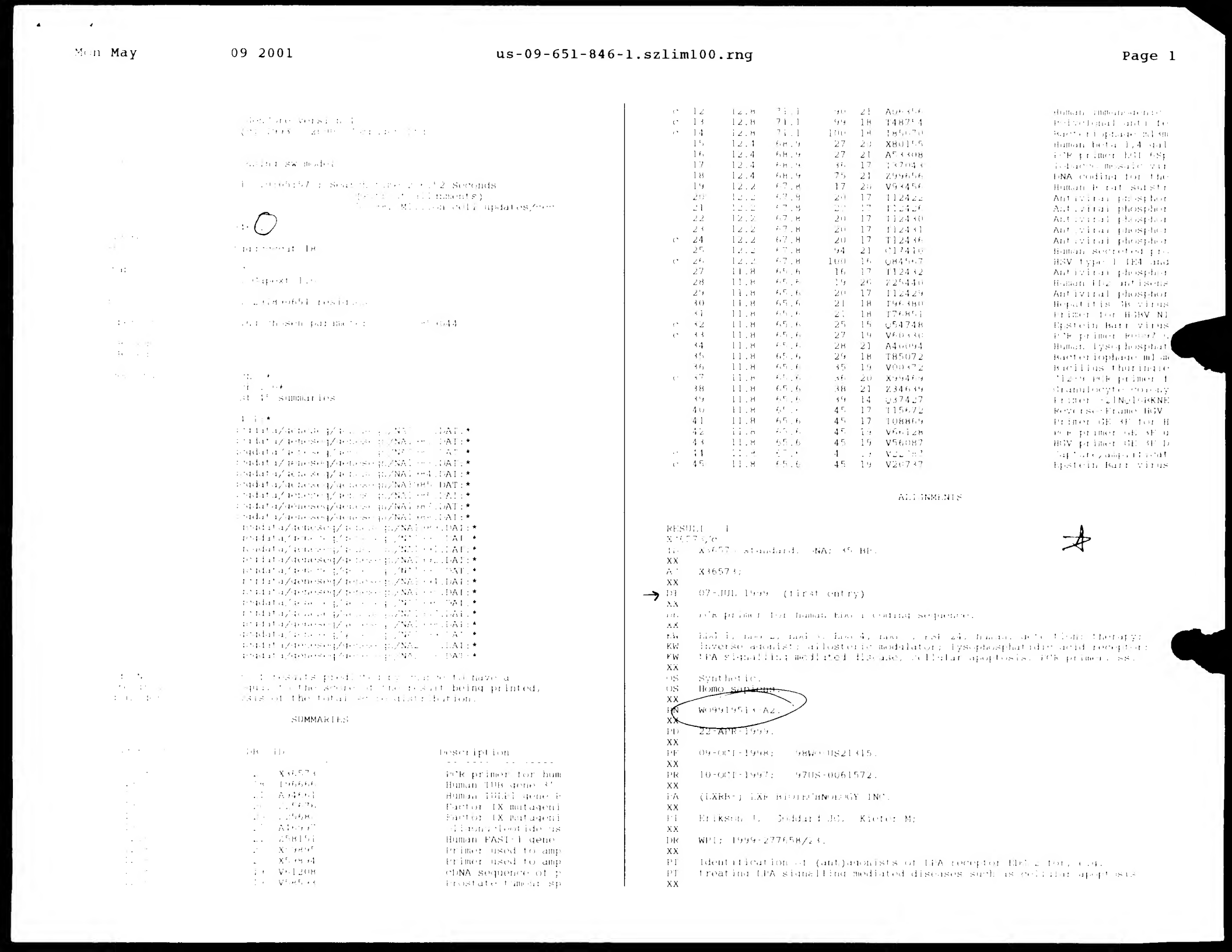

PS Example 1; Page 40; 64pp; English.
XX
CC This sequence is a PCR primer for DNA encoding human EDG 1.
CC The invention relates to methods of detecting (ant)agonist, inverse
CC agonist or allosteric modulators of the lysophosphatidic acid receptors
CC EDG-1, EDG-2, EDG-3, EDG-4, EDG-5, and PSP-24. The methods are used to
CC identify (ant)agonists and allosteric modulator of the lysophosphatidic
CC acid (LPA) EDG2 receptor, e.g. to treat LPA signalling mediated disease
CC such cellular apoptosis.
XX
SQ Sequence 45 BP; 7 A; 15 C; 12 G; 9 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.2e;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gacgctgqtqqqcccccat 18
||||||||||||||||||
Db 42 GACGCTGGTCGGGCCCCAT 25

RESULT 2
T96666/c
ID T96666 standard; cDNA; 19 BP.
XX
AC T96666;
XX
DT 27-APR-1998 (first entry)
XX
DE Human TUB gene 3' end primer for radiation hybrid mapping.
XX
KW TULP; tub gene; human; sensory neuron; neurosensory defect;
KW cochlear degeneration; hearing loss; deafness; retinal dystrophy;
KW retinitis pigmentosa; combined rod cone dystrophy; obesity;
KW animal model; transgenic animal; therapy; diagnosis; PCR; primer;
KW ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9748004 A1.
XX
PD 18-DEC-1997.
XX
PF 10-APR-1997; 97WO-US05903.
XX
PR 17-SEP-1996; 96US-0714991.
PR 10-APR-1996; 96US-0640592.
PR 22-AUG-1996; 96US-0701480.
PR 04-SEP-1996; 96US-0706292.
XX
PA (JACK-) JACKSON LAB.
PA (SEQU-) SEQUANA THERAPEUTICS INC.
XX
PI Nagaraja J, Nishina P, Naggert J, North M.
XX
DR WPI; 1997-512642/47.
XX
PT Mammalian TULP protein used for detecting pre-disposition to
PT neuro-sensory defects
XX
PS Disclosure; Page 35; 89pp; English.
XX
CC PCR primers (T96663 and T96664) were designed for the 3' non-coding
CC region of the human TUB gene (see T96639) and were used in
CC radiation hybrid mapping, generating a product of 221 bp. Another
CC primer pair (see T96661 62) amplified the 5' region of TUB, and a
CC further pair (see T96665-66) amplified TULP1 cDNA (see T96642).
CC TUB and TULP1 are novel members of the mammalian TULP gene family
CC associated with various defects in sensory neurons such as
CC cochlear defects, retinitis pigmentosa and combined rod cone
CC dystrophy.
XX
SQ Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 other;

Query Match 73.3%; Score 13.2; DB 2; Length 19;
Best Local Similarity 84.3%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 gacgctgqtqqqcccccat 18
||||||||| | ||| |||
Db 19 GACGCTGGTGGGACGCCCAT 2

RESULT 3
A94661/c
ID A94661 standard; DNA; 19 BP.
XX
AC A94661;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human TULP1 gene PCR primer #2.
XX
KW Human; TULP; neurosensory defect; retina; retinal dystrophy; PCR primer;
KW TUB; ss.
XX
OS Homo sapiens.
XX
PN US6114502-A.
XX
PD 05-SEP-2000.
XX
PF 27-FEB-1998; 98US-0032765.
XX
PR 22-AUG-1996; 96US-0701480.
PR 04-SEP-1996; 96US-0706292.
PR 10-APR-1996; 96US-0640592.
PR 17-SEP-1996; 96US-0714991.
PR 30-APR-1997; 97US-0850218.
PR 01-AUG-1997; 97US-0904699.
PR 17-SEP-1997; 97US-0932306.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI North M, Nishina P, Naben-Tranth K, Naggert J;
XX
DR WPI; 2000-586483/55.
XX
PT Mammalian proteins expressed in retina and brain, useful for producing
PT antibodies and for diagnosing neurosensory defects i.e. including cochlear
PT degeneration, peripheral retinal degeneration and cone-rod retinal
PT dystrophy -
XX
PS Disclosure; Column 26; 61pp; English.
XX
CC The present invention relates to human and murine cDNAs from a
CC neurosensory defect associated gene family. The novel cDNAs are mouse tub
CC form 1 (see A94629), mouse tub form 11 (see A94630), human TUB form 6
CC (see A94632), human TUB form 1 (see A94633), human TULP1 (see A94635),
CC human TULP2 (see A94636), human TULP3 (see A94637) and mouse TULP4 (see
CC A94638). The novel coding sequences are useful as immunogens to raise
CC [illegible] specifically identify TULP/TUP-expressing cells and in
CC drug screening assays directed at neurosensory defects. The novel
CC proteins encoded by the present sequence can be used for the treatment of
CC neurosensory degenerative conditions e.g. retinal dystrophies. The
CC present sequence is a PCR primer used to isolate the novel genes of the
CC present invention.
XX
SQ Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 other;

Query Match 73.3%; Score 13.2; DB 2; Length 19;
Best Local Similarity 84.3%; Pred. No. 1.3e+04;

[illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible] predicted Factor IXa (Ser365-Ala).

[illegible] mutagenic [illegible] thrombosis;
[illegible] blood circulation [illegible] surgery;
[illegible] bypass [illegible]
[illegible] ss.

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible] patient subjected to extra corporeal blood

[illegible]

[illegible] English.

[illegible] bed for inhibiting the process in a patient whose
[illegible] extra corporeal blood circulation. The method
[illegible] mixing the extra corporeal circulating blood
[illegible] and (2). The method is used when the patient
[illegible] extra corporeal blood circulation during
[illegible] portal surgery, vascular surgery or
[illegible] artery. The present [illegible] represents a
[illegible] the production of a mutated Factor IX, in the
[illegible] present invention.

[illegible]

[illegible]

[illegible]

[illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

XX
DE Factor IX mutagenic primer for producing Factor IXa (Ser365 Ala).
XX
KW Factor IX; Factor IXmi; mutant; mutagenic primer; ischaemia; stroke;
KW ischaemic disorder; Factor IXa; fibrinolytic; inhibition; coagulation;
KW peripheral vascular disorder; pulmonary embolus; venous thrombosis;
KW myocardial infarction; transient ischaemic attack; unstable angina;
KW reversible ischaemic neurological deficit; sickle cell anaemia;
KW organ transplantation surgery; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9949880-A1.
XX
PD 07-OCT-1999.
XX
PF 01-APR-1999; 99WO-US07175.
XX
PR 01-APR-1998; 98US-0053871.
XX
PA (UYOO) UNIV COLUMBIA NEW YORK.
XX
PI Pinsky DJ, Stern D, Schmidt AM, Rose L, Scott [illegible]
XX
DR WPI; 1999-612457/51.
XX
PT Treating ischaemic disorders and improving stroke [illegible] by using a Factor
PT IXa
XX
PS Disclosure; Page 26; 174pp; English.
XX
CC The present invention describes a method for treating an ischaemic
CC disorder by administering a Factor IXa compound and optionally an
CC indirect or direct fibrinolytic agent, to inhibit coagulation.
CC Preferably Factor IXa compound is an active site-blocked Factor
CC IXa or a Glu-Gly-Arg chloromethyl ketone inactivated human Factor IXa.
CC This and other forms of the factor may be used to treat an ischaemic
CC disorder in a mammal, especially a human. The disorder may be a
CC peripheral vascular disorder, a pulmonary embolus, a venous thrombosis,
CC a myocardial infarction, a transient ischaemic attack, unstable angina,
CC a reversible ischaemic neurological deficit, sickle cell anaemia or a
CC stroke disorder. The ischaemic disorder may be intravenously induced.
CC The subject may also be undergoing angioplasty, heart, lung, spinal,
CC brain, vascular, abdominal or organ transplantation surgery. The present
CC sequence represents a mutagenic primer used in the production of a
CC mutated Factor IX, in the exemplification of the present invention.
XX
SQ Sequence 30 BP; 5 A; 11 C; 7 G; 7 T; 0 other;

Query Match 73.3%; Score 15.2; DB 2; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches [illegible]; Indels [illegible] Gaps [illegible]

Qy 1 gagcctattgaccccat 18
[illegible]
Db 19 GAGCCTGGGGGAGCCCAT 2

RESULT 6
A46997/c
ID A46997 standard; cDNA; 48 BP.
XX
AC A46997;
XX
DT 03-OCT-2000 (first entry)
XX
DE Oligonucleotide used for in situ analysis of IF-8 cDNA
XX
KW PR0291; PR0292; PR0327; PR1265; PR0344; PR0347; PR0347;
KW PR0715; PR0817; PR0112; PR0509; PR0855; PR0884; tumour cell; probe;
KW tumourigenesis; cancer; neoplastic cell growth; cell proliferation; ss.

XX
OS Homo sapiens.
XX
PN WO200047640-A2.
XX
PD 17-AUG-2000.
XX
PF 16-DEC-1999; 99WO-US30095.
XX
PR 22-DEC-1998; 98US-0113296.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28413.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28401.
PR 02-DEC-1999; 99WO-US28565.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, May MA,
PI Wood WI;
XX
DR WPI; 2000-452188/39.
XX
PT New anti-polypeptide antibody useful in the treatment and diagnosis of
PT neoplastic cell growth and proliferation -
XX
PS Example 18; Page 153; 220pp; English.
XX
CC The present sequence was used for in situ analysis of DNA encoding
CC a novel human polypeptide. The specification describes novel polypeptides
CC designated PRO201, PRO292, PRO327, PRO326, PRO341, PRO343, PRO347,
CC PRO357, PRO715, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These
CC genes are amplified in the genome of tumour cells. The polypeptides
CC are believed to contribute to tumourigenesis. The polypeptides are
CC useful target for the identification of certain cancers, and may act
CC as predictors of the prognosis of tumour treatment. Antibodies against
CC these polypeptides are useful in the treatment and diagnosis of
CC neoplastic cell growth and proliferation in mammals.
XX
SQ Sequence 48 BP; 16 A; 12 C; 12 G; 8 T; 0 other;

Query Match 73.4%; Score 13.2; DB 21; Length 48;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 qacgctcgtqtqqqcccccat 18
|| ||||| ||||||| ||
Db 38 GCCGCTGTTGGGCCCTAT 21

RESULT 7
Z58151/c
ID Z58151 standard; DNA; 41 BP.
XX
AC Z58151;
XX
DT 25-APR-2000 (first entry)
XX
DE Human FAST-1 gene PCR primer NT2 exp5'.
XX
KW FAST-1; hFAST-1; human; forkhead activin signal transducer;
KW signal transduction; tumour-derived growth factor-beta; TGF beta;
KW activin; tumour; therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO9902910-A2.
XX
PD 21-JAN-1999.

XX
PF 18-JUN-1999; 99WO-US13764.
XX
PR 10-JUL-1998; 98US-0113309.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Zhou S, Kamel L, Vogelstein B, Kinzler KW;
XX
DR WPI; 2000-163807/14.
XX
PT Novel human forkhead activin signal transducer gene and polypeptides,
PT used for screening for compounds which modulate the action of TGFbeta
PT -
XX
PS Example 6; Page 22; 47pp; English.
XX
CC The present sequence is that of primer NT2 exp5', which was used
CC in the PCR amplification of human full-length FAST-1 (hFAST-1)
CC open reading frame (see Z58144) using human colon cDNA as template.
CC The PCR product was used in the construction of an expression
CC vector that was utilised in experiments to demonstrate hFAST-1
CC mediated transcriptional activation. hFAST-1 (see Y98744) mediates
CC transcriptional responses to tumour derived growth factor beta
CC (TGF-beta) and activin in a ligand-, receptor- and Smad dependent
CC fashion. The invention includes tools for investigating the
CC TGF beta signalling pathway, and screening for compounds which
CC modulate the action of TGF-beta. Such compounds can be used to
CC modify or regulate transcriptional activation associated with the
CC TGF-beta signalling pathway, and can be applied therapeutically to
CC alter the growth of tumour cells, or to alter normal or abnormal
CC developmental responses.
XX
SQ Sequence 41 BP; 3 A; 12 C; 11 G; 4 T; 0 other;

Query Match 71.1%; Score 12.8; DB 21; Length 41;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 cgctqqtqqqcccccat 18
|||||| |||||||||
Db 31 CGCTGCAGGGCCCCAT 16

RESULT 8
X59895/c
ID X59895 standard; DNA; 33 BP.
XX
AC X59895;
XX
DT 29-JUL-1999 (first entry)
XX
DE Primer used to amplify N terminal deletion inserts of PR3 cDNA.
XX
KW Human proteinase 3; PR3; antibody; alveolar haemorrhage;
KW PR3-specific anti-neutrophil cytoplasmic autoantibody;
KW biopsy proven; Wegener's granulomatosis; WG; vasculitis;
KW necrotizing granulomatous lesion; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9925738-A1.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-US24333.
XX
PR 13-NOV-1997; 97US-0969238.
XX
PA (MAYO) MAYO FOUNDATION.
XX
PI Fass DN, Jenne DE, Specks U;

[illegible]

[illegible] t-1 detecting [illegible] severe
[illegible] hemorrhage

[illegible] English.

[illegible] used to amplify cDNA [illegible] encoding
[illegible] proteinase 3 (PR3), an identification
[illegible] the specific binding affinity for PR3, that
[illegible] specific anti neutrophil cytoplasmic
[illegible] by proven Wegener's granulomatosis (WG)
[illegible] bind to PR3. The cells used in inactivated
[illegible] a substrate for PR3 specific antineutrophil
[illegible] (ANCA). Cells expressing the inactive human
[illegible] are easier to culture than those expressing
[illegible] detected. Of antibodies bound cytoplasmic
[illegible] recombinant PR3 are indicative of disease
[illegible] or severe disease, such as alveolar
[illegible] an active disease typically, contain ANCA that
[illegible] mature and pro-form PR3. Patients having
[illegible] contain ANCA that specifically bind only to
[illegible] alveolar hemorrhage can be distinguished from
[illegible] as lesions.

[illegible] 71.1%; Score 12.8; DB 20; Length 33;
Best Local Similarity [illegible] 87.5%; Pred. No. 2e-04;
Matches 14; [illegible] 0; Mismatches 2; Indels 0; Gaps 0;

[illegible]

[illegible] 90

[illegible]

[illegible] terminal deletion [illegible] cDNA.

[illegible] detecting [illegible] cytoplasmic
[illegible] granulomatosis; [illegible]
[illegible] lesion; PCR primer [illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible] t-1 detecting [illegible] severe
[illegible] hemorrhage

[illegible] English.

XX
CC PCR primers X59692-97 were used to amplify cDNA inserts encoding
CC N-terminal deletions in human proteinase 3 (PR3). The specification
CC describes an antibody, with specific binding affinity for PR3, that
CC does not compete with PR3-specific anti-neutrophil cytoplasmic
CC autoantibodies from biopsy-proven Wegener's granulomatosis (WG)
CC patients for specific binding to PR3. The methods use an inactivated
CC human PR3 (PR3-S176A) as a substrate for PR3 specific anti neutrophil
CC cytoplasmic autoantibodies (ANCA). Cells expressing the inactive human
CC PR3 appear healthier and are easier to culture than those expressing
CC an active PR3 version. Detection of anti neutrophil cytoplasmic
CC autoantibodies bound to recombinant PR3 are indicative of disease
CC activity such as vasculitis, or severe disease, such as alveolar
CC hemorrhage. Patients having active disease contain ANCA that
CC specifically bind to both mature and proform PR3. Patients having
CC inactive disease typically, contain ANCA that specifically bind only to
CC mature form PR3. Hence alveolar hemorrhage can be distinguished from,
CC e.g. necrotizing granulomatous lesions.
XX
SQ Sequence 33 BP; 4 A; 12 C; 10 G; 7 T; 0 other;

Query Match 71.1%; Score 12.8; DB 20; Length 33;
Best Local Similarity 87.5%; Pred. No. 2e-04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gacgctcatgaggccc 16
||||| ||||| |||
Db 13 gacgccaatgaccccc 28

RESULT 10
V61208/c
ID V61208 standard; cDNA; 90 BP.
XX
AC V61208;
XX
DT 06-JAN-1999 (first entry)
XX
DE cDNA sequence of prostate tumour clone.
XX
KW Prostate; cancer; tumour; vaccine; immunodet; [illegible] ss.
XX
OS Homo sapiens.
XX
PN WO9847993-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US003492.
XX
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
DR WPI; 1998-609886/51.
XX
PT Polypeptides comprising immunogenic portions of prostate proteins
PT used in a vaccine for the treatment of prostate cancer
XX
PS Claim 3; Page 87; 140pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX

```
SQ   Sequence 90 BP; 13 A; 29 C; 28 G; 19 T; 1 other;

  Query Match             71.1%;  Score 12.8;  DB 19;  Length 90;
  Best Local Similarity   87.5%;  Pred. No. 2.1e-03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 gacgctgqtqtqqcccc 16
           ||| |||| |||||||
Db      31 GACTCTGGGGGGCCCC 16


RESULT  11
V58593/c
ID   V58593 standard; cDNA; 90 BP.
XX
AC   V58593;
XX
DT   08-DEC-1998  (first entry)
XX
DE   Prostate tumour specific gene clone.
XX
KW   Prostate tumour specific gene; human; prostate cancer; detection;
KW   therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9837418-A2.
XX
PD   27-AUG-1998.
XX
PF   25-FEB-1998;   98WO-US03690
XX
PR   09-FEB-1998;   98US-0904809.
PR   25-FEB-1997;   97US-0806596.
PR   01-AUG-1997;   97US-0904809.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Dillon DC,  Xu J;
XX
DR   WPI; 1998-480805/41.
XX
PT   Novel human prostate specific tumour protein and fragments  useful
PT   for detecting and treating prostate cancers.
XX
PS   Claim 1; Page 92; 141pp; English.
XX
CC   This sequence represents a human prostate tumour specific gene, and can
CC   be used in the method of the invention. The method is for detecting
CC   prostate cancer comprises contacting a biological sample with an agent
CC   able to bind an immunogenic portion of a prostate protein (such as
CC   encoded by this sequence). An antibody which binds to an immunogenic
CC   portion of the prostate protein, and the method can be used to detect,
CC   monitor progression of, or treat prostate cancers. The antibody may
CC   also be conjugated to a therapeutic agent for use in therapy of prostate
CC   cancers.
XX
SQ   Sequence 90 BP; 13 A; 29 C; 28 G; 19 T; 1 other;


  Query Match             71.1%;  Score 12.8;  DB 19;  Length 90;
  Best Local Similarity   87.5%;  Pred. No. 2.1e-03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 gacgctgqtqqqcccc 16
           ||| |||| |||||||
Db      31 GACTCTGGGGGGCCCC 16


RESULT  12
A06356/c
ID   A06356 standard; cDNA; 90 BP.
XX
AC   A06356;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:1420.
XX
KW   Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW   immunogenic; cytostatic; vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200004149-A2.
XX
PD   27-JAN-2000.
XX
PF   14-JUL-1999;   99WO-US15838.
XX
PR   14-JUL-1998;   98US-0115453.
PR   14-JUL-1998;   98US-0116114.
PR   23-SEP-1998;   98US-0159812.
PR   23-SEP-1998;   98US-0159822.
PR   15-JAN-1999;   99US-0232149.
PR   15-JAN-1999;   99US-0232880.
PR   09-APR-1999;   99US-0288946.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Dillon DC,  Barlocker SL,  Yuqin J,  Xu J,  Mitcham JL;
XX
DR   WPI; 2000-171268/15.
XX
PT   New polypeptide useful for treating and diagnosing prostate cancer
PT   comprises an immunogenic portion of prostate tumor protein
XX
PS   Claim 1; Page 142; 263pp; English.
XX
CC   The present invention describes isolated polypeptides, comprising an
CC   immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC   and polynucleotides encoding them have cytostatic activity and can be
CC   used in vaccines and in gene therapy. The polypeptides and
CC   polynucleotides encoding them, antigen presenting cells which express
CC   the polypeptides, antibodies against the polypeptides and vaccines
CC   comprising them can be used for inhibiting the development of prostate
CC   cancer in a patient. The polypeptides can be used to generate antibodies
CC   or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC   the polynucleotides encoding the polypeptides can be used as a probe or
CC   to modulate the expression of the polypeptides. A06241 to A06691 and
CC   Y82000 to Y82020 represent sequences used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 90 BP; 13 A; 29 C; 28 G; 19 T; 1 other;


  Query Match             71.1%;  Score 12.8;  DB 21;  Length 90;
  Best Local Similarity   87.5%;  Pred. No. 2.1e-03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 gacgctgqtqqqcccc 16
           ||| |||| |||||||
Db      31 GACTCTGGGGGGCCCC 16


RESULT  13
148754/c
ID   148754 standard; DNA; 99 BP.
XX
AC   148754;
XX
DT   07-NOV-1997  (first entry)
XX
DE   Polyclonal anti-ferritin binder sequence, A4, from F2c library DNA.
XX
```

[illegible] affinity [illegible] reactive group;
[illegible] assay; detection [illegible] analyte; Chlamydia;
[illegible] allergen; [illegible] fertility; myoglobin;
[illegible] ferritin; [illegible] chain; troponin;
[illegible] human; growth [illegible] immunoglobulin E;
[illegible] placental [illegible] hepatitis antigen;
[illegible] luteinising [illegible] cytomegalovirus;
[illegible] plasma; DK MB; [illegible] specific antigen;
alpha fetoprotein; herpes [illegible]; CA125; ss.

[illegible]

[illegible]

[illegible] of an analyte [illegible] competitor
[illegible] for detection [illegible] macromolecules

[illegible] English.

[illegible] sequence from
[illegible] which may be used [illegible] conjugate of the
[illegible] conjugate comprises at least one label
[illegible] of an analyte of interest. The
competing effectively with the analyte for a
[illegible] receptor for the analyte. The conjugate
[illegible] is altered upon interaction with the affinity
[illegible] can be measured and related to the amount of
sample. Functional [illegible] such as this have
that allows the [illegible] to compete effectively
a limiting amount of [illegible] affinity receptor.
[illegible] able to mimic naturally [illegible] analytes.
[illegible] in standard competitive affinity assays
[illegible] assays) for detection [illegible] macromolecules such
[illegible] polynucleotides, glycoproteins and
[illegible], as well as small haptens. Typical
[illegible] detection include [illegible] tumour markers,
[illegible] to fertility-pregnancy [illegible] analytes associated
In particular, the assays are useful for
[illegible] stimulating [illegible] growth hormone
[illegible] parathyroid [illegible] placental
[illegible] antibodies [illegible] human
[illegible] luteinising [illegible] cytomegalovirus,
[illegible] herpes virus, CK-MB,
[illegible] troponin [illegible] antigen,
[illegible] specific [illegible] (a tumour marker).

[illegible]

[illegible]%; Score 12.8; [illegible] Length 99;
[illegible]%; Pred. No. 2.[illegible]
[illegible] Mismatches [illegible] Indels 0; Gaps 0;

[illegible]

```
                  |||||||||  |
Db         33 GACG[illegible] 18

RESULT 14
I85070/c
ID   I85070 standard; DNA; 100 BP.
XX
AC   I85070;
XX
DT   19-MAR-1998  (first entry)
XX
DE   Bacteriophage m13mp18 oligonucleotide used in helicase assay.
XX
KW   Bacteriophage m13mp18 cloning vector; helicase assay; antiviral;
KW   human cytomegalovirus primase; HCMV; screening; inhibitor; infection;
KW   diagnosis; ss.
XX
OS   Bacteriophage M13mp18.
XX
FH   Key                 Location/Qualifiers
FT   misc_binding        38..62
FT                       /*tag= a
FT                       /note= "Annealed to complementary oligonucleotide"
XX
PN   GB2311068-A.
XX
PD   17-SEP-1997.
XX
PF   05-MAR-1997;   97GB-0004575.
XX
PR   04-APR-1996;   96GB-0007118.
PR   14-MAR-1996;   96US-0013389.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Gotlib L,  Hazuda DJ,  Latemina RL;
XX
DR   WPI; 1997-427960/40.
XX
PT   Novel human cytomegalovirus helicase - used for screening for HCMV
PT   antivirals and in diagnosis of HCMV related diseases
XX
PS   Example 2; Page 7; 28pp; English.
XX
CC   The present sequence represents a single stranded oligonucleotide
CC   encompassing nucleotides 5865-5964 of bacteriophage m13mp18 cloning
CC   vector DNA. This is annealled with an oligonucleotide having the
CC   complementary sequence to bases 5902-5926. Klenow extension of the
CC   annealed duplex results in a partial DNA duplex which acts as a helicase
CC   substrate. The invention relates to a new human cytomegalovirus (HCMV)
CC   helicase, which is used in a screening assay for compounds that inhibit
CC   HCMV helicase (preferably with an IC50 of not more than 200nM). It
CC   is useful as a screening tool for HCMV antivirals, and as a diagnostic
CC   tool for diseases resulting from HCMV infection.
XX
SQ   Sequence 100 BP;  23 A;  30 C;  30 G;  17 T;  0 other;

  Query Match             71.1%;  Score 12.8;  DB 2;  Length [illegible];
  Best Local Similarity   87.5%;  Pred. No. 2.1e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 acgctgatgc[illegible]ca 17
              |||||||| |||||
Db         48 ACGCTGGT[illegible]CA 33

RESULT 15
X80155
ID   X80155 standard; DNA; 27 BP.
XX
AC   X80155;
```

XX
DT 17-AUG-1999 (first entry)
XX
DE Human beta-1,4-galactose transferase PCR primer #4.
XX
KW Human; beta-1,4-galactose transferase; preparation; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP11147247-A.
XX
PD 25-MAY-1999.
XX
PF 10-NOV-1997; 97JP-0306967.
XX
PR 10-NOV-1997; 97JP-0306967.
XX
PA (TOYM) TOYOBO KK.
XX
DR WPI; 1999-374371/32.
XX
PT Preparing beta-1,4-galactose transferase using recombinant
PT techniques
XX
PS Example 1; Page 8; 9pp; Japanese.
XX
CC A method has been developed for the preparation of human-derived
CC beta-1,4-galactose transferase. The method comprises transformation of
CC Escherichia coli by an expression vector containing a gene encoding
CC human derived beta-1,4-galactose transferase and a gene coding
CC maltose-combined protein. The transformant is cultured to form a fusion
CC protein consisting of human-derived beta-1,4 galactose transferase and
CC maltose-combined protein. The fusion protein is purified by affinity
CC chromatography and digested with enzymes to form beta 1,4-galactose
CC transferase. The method can be used to prepare human derived
CC beta-1,4-galactose transferase easily and efficiently in large amounts.
CC The present sequence represents a PCR primer for human
CC beta-1,4-galactose transferase.
XX
SQ Sequence 27 BP; 7 A; 6 C; 8 G; 6 T; 0 other;

Query Match 68.9%; Score 12.4; DB 20; Length 27;
Best Local Similarity 92.9%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ctgatgqqqcccat 18
|| |||||||||
Db 5 ctagtgqqqcccat 18

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